

1647

OIPE

#12

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/600,991

DATE: 09/07/2001

TIME: 14:13:11

Input Set : A:\0471-0162P.ST25.txt

Output Set: N:\CRF3\09072001\I600991.raw

3 <110> APPLICANT: MEDICO, Enzo  
 4 MICIELI, Paolo  
 5 COLLESI, Chiara  
 6 CASELLI, Gianfranco  
 7 COMOGLIO, Paolo  
 9 <120> TITLE OF INVENTION: RECOMBINANT PROTEINS DERIVED FROM HGF AND KSP  
 11 <130> FILE REFERENCE: 0471-0162P  
 13 <140> CURRENT APPLICATION NUMBER: US 09/600,991  
 C--> 14 <141> CURRENT FILING DATE: 2001-08-20  
 16 <160> NUMBER OF SEQ ID NOS: 22  
 18 <170> SOFTWARE: PatentIn version 3.1  
 20 <210> SEQ ID NO: 1  
 21 <211> LENGTH: 1725  
 22 <212> TYPE: DNA  
 23 <213> ORGANISM: Artificial Sequence  
 25 <220> FEATURE:  
 26 <223> OTHER INFORMATION: Magic F-1 DNA coding sequence  
 28 <400> SEQUENCE: 1

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30	ctgctcccca	tgcctatccc	ctatgcagag	ggacaaagga	aaagaagaaa	tacaattcat	120
31	gaattcaaaa	aatcagcaaa	gactacccta	atcaaaatag	atccagcact	gaagataaaa	180
32	acaaaaaaag	tgaatactgc	agaccaatgt	gctaatagat	gtactaggaa	taaaggactt	240
33	ccattcactt	gcaaggcttt	tgtttttgat	aaagcaagaa	aacaatgcct	ctggttcccc	300
34	ttcaatagca	tgtcaagtgg	agtgaaaaaa	gaatttgccc	atgaatttga	cctctatgaa	360
35	aacaaagact	acattagaaa	ctgcatcatt	ggtaaaggac	gcagctacaa	gggaacagta	420
36	tctatcacta	agagtggcat	caaatgtcag	ccctggagtt	ccatgatacc	acacgaacac	480
37	agctatcggg	gtaaagacct	acaggaaaac	tactgtcgaa	atcctcgagg	ggaagaaggg	540
38	ggaccctggt	gtttcacaag	caatccagag	gtacgctacg	aagtctgtga	cattcctcag	600
39	tgttcagaag	ttgaatgcat	gacctgcaat	ggggagagtt	atcgagggtct	catggatcat	660
40	acagaatcag	gcaagatttg	tcagcgctgg	gatcatcaga	caccacaccg	gcacaaattc	720
41	ttgcctgaaa	gatatcccga	caagggtctt	gatgataatt	attgccgcaa	tcccgatggc	780
42	cagccgaggg	catggtgcta	tactcttgac	cctcacaccc	gctgggagta	ctgtgcaatt	840
43	aaaacatgcg	ctgacaaagc	ttcgggcggt	ggcgggttctg	gtggcggttg	ctccggcggt	900
44	ggcgggttctc	tagaggggaca	aaggaaaaga	agaaatacaa	ttcatgaatt	caaaaaatca	960
45	gcaaagacta	ccctaataca	aatagatcca	gcactgaaga	taaaaaccaa	aaaagtgaat	1020
46	actgcagacc	aatgtgctaa	tagatgtact	aggaataaag	gacttccatt	cacttgcaag	1080
47	gctttttgttt	ttgataaagc	aagaaaacaa	tgcctctggt	tccccttcaa	tagcatgtca	1140
48	agtggagtga	aaaaagaatt	tggccatgaa	tttgacctct	atgaaaacaa	agactacatt	1200
49	agaaactgca	tcattggtaa	aggacgcagc	tacaagggaa	cagtatctat	cactaagagt	1260
50	ggcatcaaat	gtcagccctg	gagttccatg	ataccacacg	aacacagcta	tcggggtaaa	1320
51	gacctacagg	aaaactactg	tcgaaatcct	cgaggggaag	aagggggacc	ctggtgtttc	1380
52	acaagcaatc	cagaggtacg	ctacgaagtc	tgtgacattc	ctcagtgttc	agaagttgaa	1440
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54	atttgtcagc	gctgggatca	tcagacacca	caccggcaca	aattcttgcc	tgaaagatat	1560
55	cccagacaagg	gctttgatga	taattattgc	cgcaatcccc	atggccagcc	gaggccatgg	1620
56	tgctatactc	ttgaccctca	caccgcctgg	gagtactgtg	caattaaaac	atgcgctgac	1680
57	aaagctgacg	acgacgacaa	acaccaccac	caccaccacc	actag		1725

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## RAW SEQUENCE LISTING

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Output Set: N:\CRF3\09072001\I600991.raw

60 <210> SEQ ID NO: 2  
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 62 <212> TYPE: PRT  
 63 <213> ORGANISM: Artificial Sequence  
 65 <220> FEATURE:  
 66 <223> OTHER INFORMATION: Magic F-1 recombinant protein obtained combining hairpin loop  
 and  
 67       kringle domains of human HGF and MSP  
 69 <400> SEQUENCE: 2  
 71 Met Trp Val Thr Lys Leu Leu Pro Ala Leu Leu Leu Gln His Val Leu  
 72 1                   5                   10                   15  
 74 Leu His Leu Leu Leu Leu Pro Ile Ala Ile Pro Tyr Ala Glu Gly Gln  
 75                   20                   25                   30  
 77 Arg Lys Arg Arg Asn Thr Ile His Glu Phe Lys Lys Ser Ala Lys Thr  
 78                   35                   40                   45  
 80 Thr Leu Ile Lys Ile Asp Pro Ala Leu Lys Ile Lys Thr Lys Lys Val  
 81                   50                   55                   60  
 83 Asn Thr Ala Asp Gln Cys Ala Asn Arg Cys Thr Arg Asn Lys Gly Leu  
 84 65                   70                   75                   80  
 86 Pro Phe Thr Cys Lys Ala Phe Val Phe Asp Lys Ala Arg Lys Gln Cys  
 87                   85                   90                   95  
 89 Leu Trp Phe Pro Phe Asn Ser Met Ser Ser Gly Val Lys Lys Glu Phe  
 90                   100                   105                   110  
 92 Gly His Glu Phe Asp Leu Tyr Glu Asn Lys Asp Tyr Ile Arg Asn Cys  
 93                   115                   120                   125  
 95 Ile Ile Gly Lys Gly Arg Ser Tyr Lys Gly Thr Val Ser Ile Thr Lys  
 96                   130                   135                   140  
 98 Ser Gly Ile Lys Cys Gln Pro Trp Ser Ser Met Ile Pro His Glu His  
 99 145                   150                   155                   160  
 101 Ser Tyr Arg Gly Lys Asp Leu Gln Glu Asn Tyr Cys Arg Asn Pro Arg  
 102                   165                   170                   175  
 104 Gly Glu Glu Gly Gly Pro Trp Cys Phe Thr Ser Asn Pro Glu Val Arg  
 105                   180                   185                   190  
 107 Tyr Glu Val Cys Asp Ile Pro Gln Cys Ser Glu Val Glu Cys Met Thr  
 108                   195                   200                   205  
 110 Cys Asn Gly Glu Ser Tyr Arg Gly Leu Met Asp His Thr Glu Ser Gly  
 111                   210                   215                   220  
 113 Lys Ile Cys Gln Arg Trp Asp His Gln Thr Pro His Arg His Lys Phe  
 114 225                   230                   235                   240  
 116 Leu Pro Glu Arg Tyr Pro Asp Lys Gly Phe Asp Asp Asn Tyr Cys Arg  
 117                   245                   250                   255  
 119 Asn Pro Asp Gly Gln Pro Arg Pro Trp Cys Tyr Thr Leu Asp Pro His  
 120                   260                   265                   270  
 122 Thr Arg Trp Glu Tyr Cys Ala Ile Lys Thr Cys Ala Asp Lys Ala Ser  
 123                   275                   280                   285  
 125 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Leu  
 126                   290                   295                   300  
 128 Glu Gly Gln Arg Lys Arg Arg Asn Thr Ile His Glu Phe Lys Lys Ser  
 129 305                   310                   315                   320  
 131 Ala Lys Thr Thr Leu Ile Lys Ile Asp Pro Ala Leu Lys Ile Lys Thr

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132		325		330		335
134	Lys Lys Val Asn Thr Ala Asp Gln Cys Ala Asn Arg Cys Thr Arg Asn					
135		340		345		350
137	Lys Gly Leu Pro Phe Thr Cys Lys Ala Phe Val Phe Asp Lys Ala Arg					
138		355		360		365
140	Lys Gln Cys Leu Trp Phe Pro Phe Asn Ser Met Ser Ser Gly Val Lys					
141		370		375		380
143	Lys Glu Phe Gly His Glu Phe Asp Leu Tyr Glu Asn Lys Asp Tyr Ile					
144	385		390		395	400
146	Arg Asn Cys Ile Ile Gly Lys Gly Arg Ser Tyr Lys Gly Thr Val Ser					
147		405		410		415
149	Ile Thr Lys Ser Gly Ile Lys Cys Gln Pro Trp Ser Ser Met Ile Pro					
150		420		425		430
152	His Glu His Ser Tyr Arg Gly Lys Asp Leu Gln Glu Asn Tyr Cys Arg					
153		435		440		445
155	Asn Pro Arg Gly Glu Glu Gly Gly Pro Trp Cys Phe Thr Ser Asn Pro					
156		450		455		460
158	Glu Val Arg Tyr Glu Val Cys Asp Ile Pro Gln Cys Ser Glu Val Glu					
159	465		470		475	480
161	Cys Met Thr Cys Asn Gly Glu Ser Tyr Arg Gly Leu Met Asp His Thr					
162		485		490		495
164	Glu Ser Gly Lys Ile Cys Gln Arg Trp Asp His Gln Thr Pro His Arg					
165		500		505		510
167	His Lys Phe Leu Pro Glu Arg Tyr Pro Asp Lys Gly Phe Asp Asp Asn					
168		515		520		525
170	Tyr Cys Arg Asn Pro Asp Gly Gln Pro Arg Pro Trp Cys Tyr Thr Leu					
171		530		535		540
173	Asp Pro His Thr Arg Trp Glu Tyr Cys Ala Ile Lys Thr Cys Ala Asp					
174	545		550		555	560
176	Lys Ala Asp Asp Asp Asp Lys His His His His His His His					
177		565		570		

180 &lt;210&gt; SEQ ID NO: 3

181 &lt;211&gt; LENGTH: 1692

182 &lt;212&gt; TYPE: DNA

183 &lt;213&gt; ORGANISM: Artificial Sequence

185 &lt;220&gt; FEATURE:

186 &lt;223&gt; OTHER INFORMATION: Metron F-1 DNA coding sequence

188 &lt;400&gt; SEQUENCE: 3

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190	tcgccattga atgacttcca agtgctccgg ggcacagagc tacagcacct gctacatgcg	120
191	gtgggtgcccg ggccttggca ggaggatgtg gcagatgctg aagagtgtgc tggtcgctgt	180
192	gggcccttaa tggactgccg ggccttccac tacaacgtga gcagccatgg ttgccaaactg	240
193	ctgccatgga ctcaacactc gccccacacg aggctgcggc gttctgggcg ctgtgacctc	300
194	ttccagaaga aagactacgt acggacctgc atcatgaaca atgggggttg gtaccggggc	360
195	accatggcca cgaccgtggg tggcctgccc tgccaggctt ggagccacaa gttcccgaat	420
196	gatcacaagt acacgcccac tctccggaat ggcctggaag agaacttctg ccgtaaccct	480
197	gatggcgacc ccggaggtcc ttggtgctac acaacagacc ctgctgtgcg cttccagagc	540
198	tgcggcatca aatcctgccg ggaggccgcg tgtgtctggt gcaatggcga ggaataccgc	600
199	ggcgcggtag accgcacgga gtcagggcgc gaggtgccagc gctgggatct tcagcaccgc	660

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Input Set : A:\0471-0162P.ST25.txt

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201 cggaatcctg acggctccga gcgccatgg tgctacacta cggatccgca gatcgagcga 780
202 gagttctgtg acctcccccg ctgcgggtcc gaggcacagc cccgcctcga gggcggtggc 840
203 ggttctggtg gcggtggctc cggcggtggc ggttctctag agggacaaag gaaaagaaga 900
204 aatacaattc atgaattcaa aaaatcagca aagactaccc taatcaaaat agatccagca 960
205 ctgaagataa aaacccaaaa agtgaatact gcagaccaat gtgctaatag atgtactagg 1020
206 aataaaggac ttccattcac ttgcaaggct tttgtttttg ataaagcaag aaaacaatgc 1080
207 ctctgggttc ctttcaatag catgtcaagt ggagtgaata aagaatttgg ccatgaattt 1140
208 gacctctatg aaaacaaaga ctacattaga aactgcatca ttggtaaagg acgcagctac 1200
209 aaggaacag tatctatcac taagagtggc atcaaagtgc agccctggag ttccatgata 1260
210 ccacacgaac acagctatcg gggtaaagac ctacaggaaa actactgtcg aaatcctcga 1320
211 ggggaagaag ggggacctg gtgtttcaca agcaatccag aggtacgcta cgaagtctgt 1380
212 gacattcctc agtgttcaga agttgaatgc atgacctgca atggggagag ttatcgaggt 1440
213 ctcatggatc atacagaatc aggaagatt tgtcagcgtc gggatcatca gacaccacac 1500
214 cggcacaat tcttgctga aagatatccc gacaagggtc ttgatgataa ttattgccgc 1560
215 aatcccgatg gccagccgag gccatggtgc tatactcttg accctcacac ccgctgggag 1620
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217 caccaccact ag 1692

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220 &lt;210&gt; SEQ ID NO: 4

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222 &lt;212&gt; TYPE: PRT

223 &lt;213&gt; ORGANISM: Artificial Sequence

225 &lt;220&gt; FEATURE:

226 <223> OTHER INFORMATION: Metron F-1 recombinant protein obtained combining hairpin  
loop and

227 kringle domains of human HGF and MSP

229 &lt;400&gt; SEQUENCE: 4

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231 Met Gly Trp Leu Pro Leu Leu Leu Leu Leu Thr Gln Cys Leu Gly Val
232 1 5 10 15
234 Pro Gly Gln Arg Ser Pro Leu Asn Asp Phe Gln Val Leu Arg Gly Thr
235 20 25 30
237 Glu Leu Gln His Leu Leu His Ala Val Val Pro Gly Pro Trp Gln Glu
238 35 40 45
240 Asp Val Ala Asp Ala Glu Glu Cys Ala Gly Arg Cys Gly Pro Leu Met
241 50 55 60
243 Asp Cys Arg Ala Phe His Tyr Asn Val Ser Ser His Gly Cys Gln Leu
244 65 70 75 80
246 Leu Pro Trp Thr Gln His Ser Pro His Thr Arg Leu Arg Arg Ser Gly
247 85 90 95
249 Arg Cys Asp Leu Phe Gln Lys Lys Asp Tyr Val Arg Thr Cys Ile Met
250 100 105 110
252 Asn Asn Gly Val Gly Tyr Arg Gly Thr Met Ala Thr Thr Val Gly Gly
253 115 120 125
255 Leu Pro Cys Gln Ala Trp Ser His Lys Phe Pro Asn Asp His Lys Tyr
256 130 135 140
258 Thr Pro Thr Leu Arg Asn Gly Leu Glu Glu Asn Phe Cys Arg Asn Pro
259 145 150 155 160
261 Asp Gly Asp Pro Gly Gly Pro Trp Cys Tyr Thr Thr Asp Pro Ala Val
262 165 170 175
264 Arg Phe Gln Ser Cys Gly Ile Lys Ser Cys Arg Glu Ala Ala Cys Val

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265		180		185		190
267	Trp Cys Asn	Gly Glu Glu Tyr Arg	Gly Ala Val Asp Arg	Thr Glu Ser		
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270	Gly Arg Glu Cys Gln Arg	Trp Asp Leu Gln His	Pro His Gln His	Pro		
271		210		215		220
273	Phe Glu Pro Gly Lys Phe	Leu Asp Gln Gly Leu Asp	Asp Asn Tyr Cys			
274	225		230		235	240
276	Arg Asn Pro Asp Gly Ser	Glu Arg Pro Trp Cys Tyr	Thr Thr Asp Pro			
277		245		250		255
279	Gln Ile Glu Arg Glu Phe	Cys Asp Leu Pro Arg Cys	Gly Ser Glu Ala			
280		260		265		270
282	Gln Pro Arg Leu Glu Gly	Gly Gly Gly Ser Gly Gly	Gly Gly Ser Gly			
283		275		280		285
285	Gly Gly Gly Ser Leu Glu	Gly Gln Arg Lys Arg Arg	Asn Thr Ile His			
286		290		295		300
288	Glu Phe Lys Lys Ser Ala	Lys Thr Thr Leu Ile Lys	Ile Asp Pro Ala			
289	305		310		315	320
291	Leu Lys Ile Lys Thr Lys	Lys Val Asn Thr Ala Asp	Gln Cys Ala Asn			
292		325		330		335
294	Arg Cys Thr Arg Asn Lys	Gly Leu Pro Phe Thr Cys	Lys Ala Phe Val			
295		340		345		350
297	Phe Asp Lys Ala Arg Lys	Gln Cys Leu Trp Phe Pro	Phe Asn Ser Met			
298		355		360		365
300	Ser Ser Gly Val Lys Lys	Glu Phe Gly His Glu Phe	Asp Leu Tyr Glu			
301		370		375		380
303	Asn Lys Asp Tyr Ile Arg	Asn Cys Ile Ile Gly Lys	Gly Arg Ser Tyr			
304	385		390		395	400
306	Lys Gly Thr Val Ser Ile	Thr Lys Ser Gly Ile Lys	Cys Gln Pro Trp			
307		405		410		415
309	Ser Ser Met Ile Pro His	Glu His Ser Tyr Arg Gly	Lys Asp Leu Gln			
310		420		425		430
312	Glu Asn Tyr Cys Arg Asn	Pro Arg Gly Glu Glu Gly	Gly Pro Trp Cys			
313		435		440		445
315	Phe Thr Ser Asn Pro Glu	Val Arg Tyr Glu Val Cys	Asp Ile Pro Gln			
316		450		455		460
318	Cys Ser Glu Val Glu Cys	Met Thr Cys Asn Gly Glu	Ser Tyr Arg Gly			
319	465		470		475	480
321	Leu Met Asp His Thr Glu	Ser Gly Lys Ile Cys Gln	Arg Trp Asp His			
322		485		490		495
324	Gln Thr Pro His Arg His	Lys Phe Leu Pro Glu Arg	Tyr Pro Asp Lys			
325		500		505		510
327	Gly Phe Asp Asp Asn Tyr	Cys Arg Asn Pro Asp Gly	Gln Pro Arg Pro			
328		515		520		525
330	Trp Cys Tyr Thr Leu Asp	Pro His Thr Arg Trp Glu	Tyr Cys Ala Ile			
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333	Lys Thr Cys Ala Asp Lys	Ala Asp Asp Asp Asp	Lys His His His			
334	545		550		555	560
336	His His His					
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VERIFICATION SUMMARY

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DATE: 09/07/2001

TIME: 14:13:12

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